

SEQUENCE LISTING

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<120> MODIFIED DNA-POLYMERASE FROM CARBOXYDOTHENUS HYDROGENOFORMANS AND
ITS USE FOR COUPLED REVERSE TRANSCRIPTION AND POLYMERASE CHAIN REACTION

<130> 1803-332-999

<150> 09/204,208

<151> 1998-12-01

<150> EP 97121151.1

<151> 1997-12-02

<160> 12

<170> PatentIn version 3.0

<210> 1

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Description of artificial sequence: amplification primer

<220>

<221> misc_feature

<222> (3)..(3)

<223> any nucleotide

<220>

<221> misc_feature

<222> (9)..(9)

<223> any nucleotide

<400> 1

ccnaaayytnc araayath

18

<210> 2

<211> 15

<212> DNA

<213> Artificial

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<223> Description of artificial sequence: amplification primer

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<223> any nucleotide

<400> 2

ytcrtrcrtgn acytg

15

<210> 3

<211> 25

<212> DNA

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<223> Description of artificial sequence: amplification primer

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gggcgaagac gctatattcc tgagc

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<210> 4

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28

<210> 5

<211> 36

<212> DNA

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<223> Description of artificial sequence: amplification primer

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cgaattcaat ccattgggaaa agtagtcctg gtggat

36

<210> 6

<211> 36

<212> DNA

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<223> Description of artificial sequence: amplification primer

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cgaattcaag gatccttact tcgcttcata ccagtt

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<210> 7

<211> 39

<212> DNA

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<223> Description of artificial sequence: amplification primer

<400> 7

cggtaaaccc atggttaatt tctcctcttt aatgaattc

39

<210> 8
 <211> 39
 <212> DNA
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 <223> Description of artificial sequence: amplification primer

<400> 8
 cggaatcca tggaaaagct tgccgaacac gaaaattta 39

<210> 9
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 <212> DNA
 <213> Artificial
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 <223> Description of artificial sequence: amplification primer

<400> 9
 aattcggatg gctacgtaca tggctg 26

<210> 10
 <211> 1824
 <212> DNA
 <213> Carboxydotherrnus hydrogenoformans

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 <221> CDS
 <222> (1)..(1824)

<400> 10
 atg gaa aag ctt gcc gaa cac gaa aat tta gca aaa ata tcg aaa caa 48
 Met Glu Lys Leu Ala Glu His Glu Asn Leu Ala Lys Ile Ser Lys Gln
 1 5 10 15

tta gct aca atc ctg cgg gaa ata ccg tta gaa atc tcc ctg gaa gat 96
 Leu Ala Thr Ile Leu Arg Glu Ile Pro Leu Glu Ile Ser Leu Glu Asp
 20 25 30

tta aaa gtt aaa gaa cct aat tat gaa gaa gtt gct aaa tta ttt ctt 144
 Leu Lys Val Lys Glu Pro Asn Tyr Glu Glu Val Ala Lys Leu Phe Leu

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

35	40	45	
cac ctt gag ttt aaa agc ttt tta aaa gaa ata gaa cca aaa ata aag His Leu Glu Phe Lys Ser Phe Leu Lys Glu Ile Glu Pro Lys Ile Lys 50 55 60			192
aaa gaa tac cag gaa ggt aaa gat ttg gtg caa gtt gaa act gta gaa Lys Glu Tyr Gln Glu Gly Lys Asp Leu Val Gln Val Glu Thr Val Glu 65 70 75 80			240
acg gaa gga cag att gca gta gtt ttt agt gat gga ttt tat gtt gat Thr Glu Gly Gln Ile Ala Val Val Phe Ser Asp Gly Phe Tyr Val Asp 85 90 95			288
gac ggg gaa aaa aca aag ttt tac tct tta gac cgg ctg aat gaa ata Asp Gly Glu Lys Thr Lys Phe Tyr Ser Leu Asp Arg Leu Asn Glu Ile 100 105 110			336
gag gaa ata ttt agg aat aaa aaa att att acc gac gat gcc aaa gga Glu Glu Ile Phe Arg Asn Lys Lys Ile Ile Thr Asp Asp Ala Lys Gly 115 120 125			384
att tat cat gtc tgt tta gaa aaa ggt ctg act ttt ccc gaa gtt tgt Ile Tyr His Val Cys Leu Glu Lys Gly Leu Thr Phe Pro Glu Val Cys 130 135 140			432
ttt gat gcg cgg att gca gct tat gtt tta aac ccg gcc gac caa aat Phe Asp Ala Arg Ile Ala Ala Tyr Val Leu Asn Pro Ala Asp Gln Asn 145 150 155 160			480
ccc ggc ctc aag ggg ctt tat cta aag tat gac tta ccg gtg tat gaa Pro Gly Leu Lys Gly Leu Tyr Leu Lys Tyr Asp Leu Pro Val Tyr Glu 165 170 175			528
gat gta tct tta aac att aga ggg ttg ttt tat tta aaa aaa gaa atg Asp Val Ser Leu Asn Ile Arg Gly Leu Phe Tyr Leu Lys Lys Glu Met 180 185 190			576
atg aga aaa atc ttt gag cag gag caa gaa agg tta ttt tat gaa ata Met Arg Lys Ile Phe Glu Gln Glu Gln Glu Arg Leu Phe Tyr Glu Ile 195 200 205			624
gaa ctt cct tta act cca gtt ctt gct caa atg gag cat acc ggc att Glu Leu Pro Leu Thr Pro Val Leu Ala Gln Met Glu His Thr Gly Ile 210 215 220			672
cag gtt gac cgg gaa gct tta aaa gag atg tcg tta gag ctg gga gag Gln Val Asp Arg Glu Ala Leu Lys Glu Met Ser Leu Glu Leu Gly Glu 225 230 235 240			720
caa att gaa gag tta atc cgg gaa att tat gtg ctg gcg ggg gaa gag Gln Ile Glu Glu Leu Ile Arg Glu Ile Tyr Val Leu Ala Gly Glu Glu 245 250 255			768
ttt aac tta aac tcg ccc agg cag ctg gga gtt att ctt ttt gaa aaa Phe Asn Leu Asn Ser Pro Arg Gln Leu Gly Val Ile Leu Phe Glu Lys 260 265 270			816
ctt ggg ctg ccg gta att aaa aag acc aaa acg ggc tac tct acc gat Leu Gly Leu Pro Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Asp 275 280 285			864
gcg gag gtt ttg gaa gag ctc ttg cct ttc cac gaa att atc ggc aaa Ala Glu Val Leu Glu Glu Leu Leu Pro Phe His Glu Ile Ile Gly Lys 290 295 300			912

300

ata Ile 305	ttg Leu	aat Asn	tac Tyr	cgg Arg 310	cag Gln	ctt Leu	atg Met	aag Lys	tta Leu	aaa Lys 315	tcc Ser	act Thr	tat Tyr	act Thr	gac Asp 320	960
ggc Gly	tta Leu	atg Met	cct Pro	tta Leu 325	ata Ile	aat Asn	gag Glu	cgt Arg	acc Thr 330	ggt Gly	aaa Lys	ctt Leu	cac His	act Thr 335	act Thr	1008
ttt Phe	aac Asn	cag Gln	acc Thr 340	ggt Gly	act Thr	tta Leu	acc Thr	gga Gly 345	cgc Arg	ctg Leu	gcg Ala	tct Ser	tcg Ser 350	gag Glu	ccc Pro	1056
aat Asn	ctc Leu	caa Gln 355	aat Asn	att Ile	ccc Pro	atc Ile	cgg Arg 360	ttg Leu	gaa Glu	ctc Leu	ggt Gly 365	cgg Arg	aaa Lys	tta Leu	cgc Arg	1104
aag Lys	atg Met 370	ttt Phe	ata Ile	cct Pro	tca Ser	ccg Pro 375	ggg Gly	tat Tyr	gat Asp	tat Tyr	att Ile 380	gtt Val	tcg Ser	gcg Ala	gat Asp	1152
tat Tyr 385	tcc Ser	cag Gln	att Ile	gaa Glu 390	tta Leu	agg Arg	ctt Leu	ctt Leu	gcc Ala	cat His 395	ttt Phe	tcc Ser	gaa Glu	gag Glu	ccc Pro 400	1200
aag Lys	ctt Leu	att Ile	gaa Glu 405	gct Ala Tyr	tac Tyr	caa Gln	aaa Lys	ggg Gly 410	gag Glu	gat Asp	att Ile	cac His	cgg Arg	aaa Lys 415	acg Thr	1248
gcc Ala	tcc Ser	gag Glu 420	gtg Val	ttc Phe	ggt Gly	gta Val	tct Ser	ttg Leu 425	gaa Glu	gaa Glu	gtt Val	act Thr	ccc Pro 430	gag Glu	atg Met	1296
cgc Arg	gct Ala	cat His 435	gcc Ala	aag Lys	tcg Ser	gtg Val	aac Asn 440	ttc Phe	ggc Gly	att Ile	gtt Val	tat Tyr 445	ggc Gly	att Ile	agt Ser	1344
gat Asp	ttt Phe 450	ggt Gly	tta Leu	ggc Gly	aga Arg	gac Asp 455	tta Leu	aag Lys	att Ile	ccc Pro	cgg Arg 460	gag Glu	gtt Val	gcc Ala	ggt Gly	1392
aag Lys 465	tac Tyr	att Ile	aaa Lys	aat Asn	tat Tyr 470	ttt Phe	gcc Ala	aac Asn	tat Tyr	ccc Pro 475	aaa Lys	gtg Val	cgg Arg	gag Glu	tat Tyr 480	1440
ctc Leu	gat Asp	gaa Glu	ctt Leu	gtc Val 485	cgt Arg	acg Thr	gca Ala	aga Arg	gaa Glu 490	aag Lys	gga Gly	tat Tyr	gtg Val	acc Thr 495	act Thr	1488
tta Leu	ttt Phe	ggg Gly 500	cga Arg	aga Arg	cgc Arg	tat Tyr	att Ile	cct Pro 505	gag Glu	cta Leu	tct Ser	tca Ser	aaa Lys 510	aac Asn	cgc Arg	1536
acg Thr	gtt Val	cag Gln 515	ggt Gly	ttt Phe	ggc Gly	gaa Glu	agg Arg 520	acg Thr	gcc Ala	atg Met	aat Asn	act Thr 525	ccc Pro	ctt Leu	cag Gln	1584
ggc Gly	tcg Ser 530	gct Ala	gcc Ala	gat Asp	att Ile	att Ile 535	aag Lys	ctt Leu	gca Ala	atg Met	att Ile 540	aat Asn	gta Val	gaa Glu	aaa Lys	1632
gaa Glu	ctt Leu	aaa Lys	gcc Ala	cgt Arg	aag Lys	ctt Leu	aag Lys	tcc Ser	cgg Arg	ctc Leu	ctt Leu	ctt Leu	tcg Ser	gtg Val	cac His	1680

545	550	555	560	
gat gag tta gtt tta gaa gtg ccg gcg gaa gag ctg gaa gag gta aaa				1728
Asp Glu Leu Val Leu Glu Val Pro Ala Glu Glu Leu Glu Glu Val Lys	565	570	575	
gcg ctg gta aaa ggg gtt atg gag tcg gtg gtt gaa ctg aaa gtg cct				1776
Ala Leu Val Lys Gly Val Met Glu Ser Val Val Glu Leu Lys Val Pro	580	585	590	
tta atc gct gaa gtt ggt gca ggc aaa aac tgg tat gaa gcg aag taa				1824
Leu Ile Ala Glu Val Gly Ala Gly Lys Asn Trp Tyr Glu Ala Lys	595	600	605	

<210> 11

<211> 607

<212> PRT

<213> Carboxydotherrmus hydrogenoformans

<400> 11

Met Glu Lys Leu Ala Glu His Glu Asn Leu Ala Lys Ile Ser Lys Gln
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Leu Ala Thr Ile Leu Arg Glu Ile Pro Leu Glu Ile Ser Leu Glu Asp
20 25 30

Leu Lys Val Lys Glu Pro Asn Tyr Glu Glu Val Ala Lys Leu Phe Leu
35 40 45

His Leu Glu Phe Lys Ser Phe Leu Lys Glu Ile Glu Pro Lys Ile Lys
50 55 60

Lys Glu Tyr Gln Glu Gly Lys Asp Leu Val Gln Val Glu Thr Val Glu
65 70 75 80

Thr Glu Gly Gln Ile Ala Val Val Phe Ser Asp Gly Phe Tyr Val Asp
85 90 95

Asp Gly Glu Lys Thr Lys Phe Tyr Ser Leu Asp Arg Leu Asn Glu Ile
100 105 110

Glu Glu Ile Phe Arg Asn Lys Lys Ile Ile Thr Asp Asp Ala Lys Gly
115 120 125

Ile Tyr His Val Cys Leu Glu Lys Gly Leu Thr Phe Pro Glu Val Cys
130 135 140

Phe Asp Ala Arg Ile Ala Ala Tyr Val Leu Asn Pro Ala Asp Gln Asn

145		150		155		160
Pro Gly Leu Lys Gly Leu Tyr Leu Lys Tyr Asp Leu Pro Val Tyr Glu	165		170		175	
Asp Val Ser Leu Asn Ile Arg Gly Leu Phe Tyr Leu Lys Lys Glu Met	180		185		190	
Met Arg Lys Ile Phe Glu Gln Glu Gln Glu Arg Leu Phe Tyr Glu Ile	195		200		205	
Glu Leu Pro Leu Thr Pro Val Leu Ala Gln Met Glu His Thr Gly Ile	210		215		220	
Gln Val Asp Arg Glu Ala Leu Lys Glu Met Ser Leu Glu Leu Gly Glu	225		230		235	240
Gln Ile Glu Glu Leu Ile Arg Glu Ile Tyr Val Leu Ala Gly Glu Glu	245		250		255	
Phe Asn Leu Asn Ser Pro Arg Gln Leu Gly Val Ile Leu Phe Glu Lys	260		265		270	
Leu Gly Leu Pro Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Asp	275		280		285	
Ala Glu Val Leu Glu Glu Leu Leu Pro Phe His Glu Ile Ile Gly Lys	290		295		300	
Ile Leu Asn Tyr Arg Gln Leu Met Lys Leu Lys Ser Thr Tyr Thr Asp	305		310		315	320
Gly Leu Met Pro Leu Ile Asn Glu Arg Thr Gly Lys Leu His Thr Thr	325		330		335	
Phe Asn Gln Thr Gly Thr Leu Thr Gly Arg Leu Ala Ser Ser Glu Pro	340		345		350	
Asn Leu Gln Asn Ile Pro Ile Arg Leu Glu Leu Gly Arg Lys Leu Arg	355		360		365	
Lys Met Phe Ile Pro Ser Pro Gly Tyr Asp Tyr Ile Val Ser Ala Asp	370		375		380	
Tyr Ser Gln Ile Glu Leu Arg Leu Leu Ala His Phe Ser Glu Glu Pro	385		390		395	400
Lys Leu Ile Glu Ala Tyr Gln Lys Gly Glu Asp Ile His Arg Lys Thr						

405

410

415

Ala Ser Glu Val Phe Gly Val Ser Leu Glu Glu Val Thr Pro Glu Met
420 425 430

Arg Ala His Ala Lys Ser Val Asn Phe Gly Ile Val Tyr Gly Ile Ser
435 440 445

Asp Phe Gly Leu Gly Arg Asp Leu Lys Ile Pro Arg Glu Val Ala Gly
450 455 460

Lys Tyr Ile Lys Asn Tyr Phe Ala Asn Tyr Pro Lys Val Arg Glu Tyr
465 470 475 480

Leu Asp Glu Leu Val Arg Thr Ala Arg Glu Lys Gly Tyr Val Thr Thr
485 490 495

Leu Phe Gly Arg Arg Arg Tyr Ile Pro Glu Leu Ser Ser Lys Asn Arg
500 505 510

Thr Val Gln Gly Phe Gly Glu Arg Thr Ala Met Asn Thr Pro Leu Gln
515 520 525

Gly Ser Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asn Val Glu Lys
530 535 540

Glu Leu Lys Ala Arg Lys Leu Lys Ser Arg Leu Leu Leu Ser Val His
545 550 555 560

Asp Glu Leu Val Leu Glu Val Pro Ala Glu Glu Leu Glu Glu Val Lys
565 570 575

Ala Leu Val Lys Gly Val Met Glu Ser Val Val Glu Leu Lys Val Pro
580 585 590

Leu Ile Ala Glu Val Gly Ala Gly Lys Asn Trp Tyr Glu Ala Lys
595 600 605

<210> 12

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Description of artificial sequence: amplification primer

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